AMENDMENTS TO THE CLAIMS

Following is the list of claims and their status:

1-27 (Canceled)

28. (Currently Amended): ~~A~~ An isolated nucleic acid ~~in isolated form,~~ comprising a sequence encoding a ~~wherein the nucleic acid encodes a protein which is homologous to the protein encoded by the~~ *PLAG1* (pleomorphic adenoma gene 1) protein ~~gene~~, wherein the amino acid ~~cDNA~~ sequence ~~corresponding to said~~ of the *PLAG1* ~~gene~~ protein is the sequence translated from the nucleic acid sequence as represented in SEQ ID NO: 116 starting with the ATG at position 481 to 483 of said nucleic acid sequence, or a fragment thereof which can be used to diagnose cells having a non-physiological proliferative capacity ~~depicted in figure 4A (SEQ ID NO: 116), and wherein a protein encoded by the nucleic acid comprises a polypeptide sequence which is at least 75% identical to the polypeptide sequence encoded by *PLAG1* in the region from zinc fingers 4 to 7 as represented in SEQ ID NOs: 120 to 123, or a complementary or antisense version of the nucleic acid~~.

29. (Currently Amended): The nucleic acid as claimed in claim ~~47~~ 28, comprising the nucleotide sequence of the *PLAG1* gene as depicted in figure 4A (SEQ ID NO: 116), or a complementary or antisense version of the nucleic acid.

30-31 (Canceled)

32. (Previously Presented): The nucleic acid as claimed in claim 47 wherein the nucleic acid is labeled.

33. (Currently Amended): A macromolecule comprising a nucleic acid in isolated form, comprising a sequence encoding a ~~a fusion of at least two of an oligonucleotide, a polynucleotide and a gene, wherein at least a first one of said oligonucleotide, polynucleotide or gene comprises a nucleotide sequence of at least one exon consisting of the~~ *PLAG1* (pleomorphic adenoma gene 1) ~~gene, and~~ protein, wherein the

amino acid sequence of the PLAG1 ~~[gene]~~ protein is the sequence translated from the nucleic acid sequence as represented in SEQ ID NO: 116 starting with the ATG at position 481 to 483 of said nucleic acid sequence, or a fragment thereof which can be used to diagnose cells having a non-physiological proliferative capacity. ~~at least a second one of said oligonucleotide, polynucleotide or gene comprises at least one exon of the *CTNNB1* (ß catenin) gene, or complementary or antisense versions of the nucleotide sequence~~.

34. (Previously Presented): The macromolecule as claimed in claim 33, wherein the nucleic acid is selected from the group consisting of:

a) a transcript corresponding to the nucleic acid;

b) cDNA corresponding to the nucleic acid; and

c) sense or antisense DNA corresponding to the nucleic acid.

35. (Previously Presented): The macromolecule as claimed in claim 34, wherein the nucleic acid is labeled.

36. (Previously Presented): A diagnostic kit comprising one of the labeled nucleic acid as claimed in claim 26 and a labeled macromolecule derivative of the nucleic acid and one or more diagnostic reagents.

37. (Previously Presented): The kit as claimed in claim 36, wherein the kit comprises labeled T-gene specific and tail specific PLR primers.

38. (Previously Presented): The kit as claimed in claim 36, wherein the macromolecule is a set of labeled nucleic acid probes and the kit further comprises a restriction enzyme.

39. (Previously Presented): The kit as claimed in claim 36, wherein the macromolecule is a labeled probe for *in situ* diagnostics.

40. (Previously Presented): An *in situ* diagnostic method for diagnosing interphase and/or metaphase cells having a non-physiological proliferative capacity, comprising the steps:

a) designing a set of nucleotide probes based on a nucleic acid as claimed in claim 26, wherein at least one of the probes is hybridisable to a region of the aberrant gene substantially mapping at the same locus as a corresponding region of the wildtype gene and/or the same or another probe is hybridsable to a region of the aberrant gene mapping at a different locus than a corresponding region of the wildtype gene;

b) incubating one or more interphase or metaphase chromosomes or interphase or metaphase cells having a non-physiological proliferative capacity, with the probe(s) under hybridising conditions; and

c) visualising the hybridsation between the probe(s) and the gene.

41. (Previously Presented): A method of diagnosing cells having a non-physiological proliferative capacity, comprising the steps of:

a) taking a biopsy of a tumor to obtain cells to be diagnosed;

b) isolating a suitable T-gene-related macromolecule therefrom;

c) analysing the macromolecule thus obtained by comparison with a wildtype reference molecule.

42. (Previously Presented): The method as claimed in claim 41, comprising the steps of:

a) taking a biopsy of a tumor to obtain cells to be diagnosed;

b) extracting total RNA thereof;

c) preparing at least one first strand cDNA of the mRNA species in the total RNA extract, which cDNA comprises a suitable tail;

d) performing one of a PCR and a RT-PCR using one of a PLAG gene specific primer, a tail-specific and a partner-specific/nested primer to amplify PLAG gene specific cDNA's;

e) separating the PCR products on a gel to obtain a pattern of bands;

f) evaluating the presence of aberrant bands by comparison to wildtype bands.

43. (Previously Presented): The method as claimed in claim 41, comprising the steps of:

a) taking a biopsy of a tumor to obtain cells to be diagnosed;

b) isolating total protein therefrom;

c) separating the total protein on a gel to obtain essentially individual bands;

d) hybridising the bands thus obtained with antibodies directed against a part of the protein encoded by a remaining part of the T-gene and against a part of the protein encoded by a substitution part of the T-gene;

e) visualising the antigen-antibody reactions and establishing the presence of aberrant bands by comparison with bands from wildtype proteins.

44. (Previously Presented): The method as claimed in claim 41, comprising at least some of the following steps:

a) taking a biopsy of a tumor to obtain cells to be diagnosed;

b) isolating total DNA therefrom;

c) digesting the DNA with a restriction enzyme;

d) separating the digest thus prepared on a gel to obtain a separation pattern;

e) hybridising the separation pattern in the gel or on the blot with a labeled nucleic acid in isolated form, comprising one of an oligonucleotide, a polynucleotide and a gene having a nucleotide sequence of at least a part of a T-gene selected from the group consisting of the *PLAG* subfamily of zinc finger protein genes, the *CNNB1* gene and fusions thereof, or complementary or degenerate versions of the nucleotide sequence; and

f) visualising the hybridisations and establishing the presence of aberrant bands by comparison to wildtype bands.

45. (Previously Presented): A method for identifying a T-gene comprising the steps of:

a) preparing one of a probe and a primer of a nucleic acid as claimed in claim 26;

b) isolating a gene which hybridises to the probe or primer.

46. (Previously Presented): A method of inhibiting expression of a T-gene comprising contacting a cell with a derivative as claimed in claim 33, wherein the derivative is one of an antisense nucleic acid, a nucleic acid coding for an antisense molecule, or otherwise interferes with expression of a T-gene, and an antibody or a derivative thereof.

47. (Currently Amended): A nucleic acid in isolated form according to claim 28, ~~wherein the nucleic acid is one of an oligonucleotide, a polynucleotide and a gene comprising a sequence of at least one exon of the PLAG1 (pleomorphic adenoma gene 1) gene, or the complementary sequence or antisense version of the nucleic acid;~~ wherein the amino acid sequence of said PLAG1 fragment ~~gene encodes a protein comprising~~ comprises at least one of the zinc fingers 1 to 7 represented by the sequences as represented in SEQ ID NOs: 117 to 123.

48. (Currently Amended): A macromolecule comprising a nucleic acid in isolated form, comprising a sequence encoding ~~fusion of at least two of an oligonucleotide, a polynucleotide and a gene having a nucleotide sequence of at least one exon of~~ the promoter region of a *CTNNB1* gene ~~, or the complementary sequence or antisense versions of the nucleotide sequence~~ which can be used to diagnose cells having a non-physiological proliferative capacity.

49. (Canceled)

50. (NEW): A macromolecule according to claim 48, wherein said nucleic acid is selected from the group consisting of a transcript corresponding to the nucleic acid, a cDNA corresponding to the nucleic acid, and a sense or antisense DNA corresponding to the nucleic acid.

51. (NEW): A macromolecule comprising a nucleic acid in isolated form comprising at least one exon of the CTNNB1 gene, which can be used to diagnose cells having a non-physiological proliferative capacity.

52. (NEW): A macromolecule according to claim 51, wherein said nucleic acid is selected from the group consisting of a transcript corresponding to the nucleic acid, a cDNA corresponding to the nucleic acid, and a sense or antisense DNA corresponding to the nucleic acid.